

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/019,048A
Source: JFW/K
Date Processed by STIC: 4/7/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>10/019,048A</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input checked="" type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____ . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional , please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	

Please consult Sequence Rules
for valid format



IFW16

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/019,048A

DATE: 04/07/2006
 TIME: 10:25:46

Input Set : N:\SMITH\PTO.TS.14.txt
 Output Set: N:\CRF4\04072006\J019048A.raw

C--> 3 <140> CURRENT APPLICATION NUMBER: US/10/019,048A
 E--> 0 <160> NUMBER OF SEQ ID NOS:
 3 <170> SOFTWARE: PatentIn Vers. 3.3

see p. 5

ERRORED SEQUENCES

5 <210> SEQ ID NO: 1
 6 <211> LENGTH: 2012
 7 <212> TYPE: DNA
 8 <213> ORGANISM: Physcomitrella patens
 10 <220> FEATURE:
 11 <221> NAME/KEY: CDS
 12 <222> LOCATION: (319)..(1896)

Does Not Comply
Corrected Diskette Needed

OK see p. 3

14 <400> SEQUENCE: 1	1	5	10	
15 ccgagtcgcg gatcagccat cggccgcctg gggccgcctg cattgtgtgg gacgggttgg 60				
17 gaggaggagg cagatgcgcg ggctgtggtg gagtcgtcat ccgaggatct actgcggcaa 120				
19 tacctccggg ttttggagcg ggccaaactct gttgcggctc ggaaggctat aggttcggca 180				
21 ggagactgtt gattttatgt cggggcatt gccattgtgg agagcggggg agactcagga 240				
23 tctgtgatgt tgctgcgcg gccccgactg ccgcagagcg tctgtgtatg acgagggtgt 300				
25 tgtggagcgg cttttggaa atg gta ttc gcg ggc ggt gga ctt cag cag ggc 351				
26 Met Val Phe Ala Gly Gly Leu Gln Gln Gly				
27	1	5	10	
29 tct ctc gaa gaa aac atc gac gtc gag cac att gcc agt atg tct ctc			399	
30 Ser Leu Glu Glu Asn Ile Asp Val Glu His Ile Ala Ser Met Ser Leu				
31	15	20	25	
33 ttc agc gac ttc ttc agt tat gtg tct tca act gtt ggt tcg tgg agc			447	
34 Phe Ser Asp Phe Phe Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser				
35	30	35	40	
37 gta cac agt ata caa cct ttg aag cgc ctg acg agt aag aag cgt gtt			495	
38 Val His Ser Ile Gln Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val				
39	45	50	55	
41 tcg gaa agc gct gcc gtg caa tgt ata tca gct gaa gtt cag aga aat			543	
42 Ser Glu Ser Ala Ala Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn				
43	60	65	70	75
45 tcg agt acc cag gga act gcg gag gca ctc gca gaa tca gtc gtg aag			591	
46 Ser Ser Thr Gln Gly Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys				
47	80	85	90	
49 ccc acg aga cga agg tca tct cag tgg aag aag tcg aca cac ccc cta			639	
50 Pro Thr Arg Arg Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu				
51	95	100	105	

RAW SEQUENCE LISTING
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Input Set : N:\SMITH\PTO.TS.14.txt
Output Set: N:\CRF4\04072006\J019048A.raw

53	tca	gaa	gta	gca	gtc	cac	aac	aag	cca	agc	gat	tgc	tgg	att	gtt	gta	687
54	Ser	Glu	Val	Ala	Val	His	Asn	Lys	Pro	Ser	Asp	Cys	Trp	Ile	Val	Val	
55				110				115							120		
57	aaa	aac	aag	gtg	tat	gat	gtt	tcc	aat	ttt	gcg	gac	gag	cat	ccc	gga	735
58	Lys	Asn	Lys	Val	Tyr	Asp	Val	Ser	Asn	Phe	Ala	Asp	Glu	His	Pro	Gly	
59				125				130							135		
61	gga	tca	gtt	att	agt	act	tat	ttt	gga	cga	gac	ggc	aca	gat	gtt	ttc	783
62	Gly	Ser	Val	Ile	Ser	Thr	Tyr	Phe	Gly	Arg	Asp	Gly	Thr	Asp	Val	Phe	
63	140				145					150					155		
65	tct	agt	ttt	cat	gca	gct	tct	aca	tgg	aaa	att	ctt	caa	gac	ttt	tac	831
66	Ser	Ser	Phe	His	Ala	Ala	Ser	Thr	Trp	Lys	Ile	Leu	Gln	Asp	Phe	Tyr	
67				160				165							170		
69	att	ggt	gac	gtg	gag	agg	gtg	gag	ccg	act	cca	gag	ctg	ctg	aaa	gat	879
70	Ile	Gly	Asp	Val	Glu	Arg	Val	Glu	Pro	Thr	Pro	Glu	Leu	Leu	Lys	Asp	
71				175				180							185		
73	ttc	cga	gaa	atg	aga	gct	ctt	ttc	ctg	agg	gag	caa	ctt	ttc	aaa	agt	927
74	Phe	Arg	Glu	Met	Arg	Ala	Leu	Phe	Leu	Arg	Glu	Gln	Leu	Phe	Lys	Ser	
75				190				195							200		
77	tcg	aaa	ttg	tac	tat	gtt	atg	aag	ctg	ctc	acg	aat	gtt	gct	att	ttt	975
78	Ser	Lys	Leu	Tyr	Tyr	Val	Met	Lys	Leu	Leu	Thr	Asn	Val	Ala	Ile	Phe	
79				205				210							215		
81	gct	gcg	agc	att	gca	ata	ata	tgt	tgg	agc	aag	act	att	tca	gcg	gtt	1023
82	Ala	Ala	Ser	Ile	Ala	Ile	Ile	Cys	Trp	Ser	Lys	Thr	Ile	Ser	Ala	Val	
83	220				225				230						235		
85	ttg	gct	tca	gct	tgt	atg	atg	gct	ctg	tgt	ttc	caa	cag	tgc	gga	tgg	1071
86	Leu	Ala	Ser	Ala	Cys	Met	Met	Ala	Leu	Cys	Phe	Gln	Gln	Cys	Gly	Trp	
87				240				245							250		
89	cta	tcc	cat	gat	ttt	ctc	cac	aat	cag	gtg	ttt	gag	aca	cgc	tgg	ctt	1119
90	Leu	Ser	His	Asp	Phe	Leu	His	Asn	Gln	Val	Phe	Glu	Thr	Arg	Trp	Leu	
91				255				260							265		
93	aat	gaa	gtt	gtc	ggg	tat	gtg	atc	ggc	aac	gcc	gtt	ctg	ggg	ttt	agt	1167
94	Asn	Glu	Val	Val	Gly	Tyr	Val	Ile	Gly	Asn	Ala	Val	Leu	Gly	Phe	Ser	
95				270				275							280		
97	aca	ggg	tgg	tgg	aag	gag	aag	cat	aac	ctt	cat	cat	gct	gct	cca	aat	1215
98	Thr	Gly	Trp	Trp	Lys	Glu	Lys	His	Asn	Leu	His	His	Ala	Ala	Pro	Asn	
99				285				290							295		
101	gaa	tgc	gat	cag	act	tac	caa	cca	att	gat	aat	gat	att	gat	act	ctc	1263
102	Glu	Cys	Asp	Gln	Thr	Tyr	Gln	Pro	Ile	Asp	Glu	Asp	Ile	Asp	Thr	Leu	
103	300				305				310						315		
105	ccc	ctc	att	gcc	tgg	agc	aag	gac	ata	ctg	gcc	aca	gtt	gag	aat	aag	1311
106	Pro	Leu	Ile	Ala	Trp	Ser	Lys	Asp	Ile	Leu	Ala	Thr	Val	Glu	Asn	Lys	
107				320				325							330		
109	aca	ttc	ttg	cga	atc	ctc	caa	tac	cag	cat	ctg	ttc	ttc	atg	ggt	ctg	1359
110	Thr	Phe	Leu	Arg	Ile	Leu	Gln	Tyr	Gln	His	Leu	Phe	Phe	Met	Gly	Leu	
111				335				340							345		
113	tta	ttt	ttc	gcc	cgt	ggt	agt	tgg	ctc	ttt	tgg	agc	tgg	aga	tat	acc	1407
114	Leu	Phe	Phe	Ala	Arg	Gly	Ser	Trp	Leu	Phe	Trp	Ser	Trp	Arg	Tyr	Thr	
115				350				355							360		
117	tct	aca	gca	gtg	ctc	tca	cct	gtc	gac	agg	ttg	tgg	gag	aag	gga	act	1455

RAW SEQUENCE LISTING
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Input Set : N:\SMITH\PTO.TS.14.txt
Output Set: N:\CRF4\04072006\J019048A.raw

118 Ser Thr Ala Val Leu Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr			
119 365	370	375	
121 gtt ctg ttt cac tac ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc	1503		
122 Val Leu Phe His Tyr Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu			
123 380	385	390	395
125 cct ggt tgg aag cca tta gta tgg atg gcg gtg act gag ctc atg tcc	1551		
126 Pro Gly Trp Lys Pro Leu Val Trp Met Ala Val Thr Glu Leu Met Ser			
127 400	405	410	
129 ggc atg ctg ctg ggc ttt gta ttt gta ctt agc cac aat ggg atg gag	1599		
130 Gly Met Leu Leu Gly Phe Val Phe Val Leu Ser His Asn Gly Met Glu			
131 415	420	425	
133 gtt tat aat tcg tct aaa gaa ttc gtg agt gca cag atc gta tcc aca	1647		
134 Val Tyr Asn Ser Ser Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr			
135 430	435	440	
137 cgg gat atc aaa gga aac ata ttc aac gac tgg ttc act ggt ggc ctt	1695		
138 Arg Asp Ile Lys Gly Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu			
139 445	450	455	
141 aac agg caa ata gag cat cat ctt ttc cca aca atg ccc agg cat aat	1743		
142 Asn Arg Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn			
143 460	465	470	475
145 tta aac aaa ata gca cct aga gtg gag gtg ttc tgt aag aaa cac ggt	1791		
146 Leu Asn Lys Ile Ala Pro Arg Val Glu Val Phe Cys Lys Lys His Gly			
147 480	485	490	
149 ctg gtg tac gaa gac gta tct att gct acc ggc act tgc aag gtt ttg	1839		
150 Leu Val Tyr Glu Asp Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu			
151 495	500	505	
153 aaa gca ttg aag gaa gtc gcg gag gct gcg gca gag cag cat gct acc	1887		
154 Lys Ala Leu Lys Glu Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr			
155 510	515	520	
157 acc agt taa cagtttgg aaagcttgc aattgatctt tattctccac	1936		
158 Thr Ser			
159 525			
161 ggcagttgct tgtttgttt ggggtgaatg accgaatgta ctggcatcca ttcttctgta	1996		
163 gccatcaatt ttgaac	2012		
272 <210> SEQ ID NO: 3			
273 <211> LENGTH: 6			
274 <212> TYPE: PRT			
275 <213> ORGANISM: Unknown			
W--> 277 <220> FEATURE:			
W--> 277 <223> OTHER INFORMATION:			
W--> 277 <400> 3			
278 Ser Glu Lys Asp Glu Leu			
E--> 279 5 misaligned amino acid numbering (see item 3 on			
281 <210> SEQ ID NO: 4			
282 <211> LENGTH: 20			
283 <212> TYPE: DNA			
284 <213> ORGANISM: Unknown			
W--> 286 <220> FEATURE:			
W--> 286 <223> OTHER INFORMATION:			

(global error)

see p.6 for error explanation

some error
Error summary
sheet

see p.4

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/019,048A

DATE: 04/07/2006
TIME: 10:25:46

Input Set : N:\SMITH\PTO.TS.14.txt
Output Set: N:\CRF4\04072006\J019048A.raw

W--> 286 <400> 4
E--> 287 tggtaart ggamicayaa 20
352 <210> SEQ ID NO: 12
353 <211> LENGTH: 60
354 <212> TYPE: DNA
355 <213> ORGANISM: Unknown
W--> 357 <220> FEATURE: → see p. 6
W--> 357 <223> OTHER INFORMATION:
W--> 357 <400> 12
358 gtcgacccgc ggactagtgg gccctctaga cccggggat ccggatctgc tggctatgaa 60
W--> 371 HEINZ et al.
E--> 372 s.n. 10/019,048
E--> 373 notice to comply 03/28/2006
E--> 375 1

delete

see pp 7-8

SEQUENCE LISTING

10/019,048A

5

<1107

<1207

<1307

<1407

<1417

<1607

<170> PatentIn Vers. 3.3

Insert these
mandatory.

SEQUENCE LISTING

numerous identifiers and their responses

at beginning of sequence
listings

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/019,048A

DATE: 04/07/2006
TIME: 10:25:47

FYI

Input Set : N:\SMITH\PTO.TS.14.txt
Output Set: N:\CRF4\04072006\J019048A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
Seq#:1; Line(s) 24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43
Seq#:1; Line(s) 44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63
Seq#:1; Line(s) 64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83
Seq#:1; Line(s) 84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102
Seq#:1; Line(s) 103,104,105,106,107,108,109,110,111,112,113,114,115,116,117
Seq#:1; Line(s) 118,119,120,121,122,123,124,125,126,127,128,129,130,131,132
Seq#:1; Line(s) 133,134,135,136,137,138,139,140,141,142,143,144,145,146,147
Seq#:1; Line(s) 148,149,150,151,152,153,154,155,156,157,158,159,160,161,162
Seq#:1; Line(s) 163,164,165,166
Seq#:2; Line(s) 167,168,169,170,171,172,173,174,175,176,177,178,179,180,181
Seq#:2; Line(s) 182,183,184,185,186,187,188,189,190,191,192,193,194,195,196
Seq#:2; Line(s) 197,198,199,200,201,202,203,204,205,206,207,208,209,210,211
Seq#:2; Line(s) 212,213,214,215,216,217,218,219,220,221,222,223,224,225,226
Seq#:2; Line(s) 227,228,229,230,231,232,233,234,235,236,237,238,239,240,241
Seq#:2; Line(s) 242,243,244,245,246,247,248,249,250,251,252,253,254,255,256
Seq#:2; Line(s) 257,258,259,260,261,262,263,264,265,266,267,268,269,270,271
Seq#:2; Line(s) 272
Seq#:3; Line(s) 274,277,281
Seq#:4; Line(s) 286,290
Seq#:5; Line(s) 295,299
Seq#:6; Line(s) 304,308
Seq#:7; Line(s) 313,317
Seq#:8; Line(s) 322,326
Seq#:9; Line(s) 331,335
Seq#:10; Line(s) 340,344
Seq#:11; Line(s) 349,352
Seq#:12; Line(s) 357

Error Explainer

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:3,4,5,6,7,8,9,10,11,12

~~PatentIn 2.0 "bug":~~

~~Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses(as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.~~

6

ignore this

10/019, 048A

?

<210> 5

<211> 17

<212> DNA

<213> Unknown

needs explanation - see p. 6

<400> 5

ggraanarrt grtgyc

see p. 8

17

8

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/10/019,048A

DATE: 04/07/2006
TIME: 10:25:47

FYI

Input Set : N:\SMITH\PTO.TS.14.txt
Output Set: N:\CRF4\04072006\J019048A.raw

Use of n's or Xaa's (NEW RULES) :

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:5; N Pos. 6

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/019,048A

DATE: 04/07/2006
TIME: 10:25:47

Input Set : N:\SMITH\PTO.TS.14.txt
Output Set: N:\CRF4\04072006\J019048A.raw

L:3 M:270 C: Current Application Number differs, Missing <140> CURRENT APPLICATION NUMBER: is Added.
L:0 M:282 E: Numeric Field Identifier Missing, <160> is required.
L:0 M:282 E: Numeric Field Identifier Missing, <110> is required.
L:0 M:282 E: Numeric Field Identifier Missing, <120> is required.
L:277 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:3, <213>
ORGANISM:Unknown
L:277 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:Unknown
L:277 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3, Line#:277
L:279 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3 /
L:286 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
ORGANISM:Unknown
L:286 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Unknown
L:286 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4, Line#:286 /
L:287 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 /
L:295 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
ORGANISM:Unknown
L:295 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Unknown
L:295 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5, Line#:295
L:296 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5
L:296 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5
L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:304 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:Unknown
L:304 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Unknown
L:304 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6, Line#:304
L:313 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>
ORGANISM:Unknown
L:313 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:Unknown
L:313 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7, Line#:313
L:322 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Unknown
L:322 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Unknown
L:322 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8, Line#:322
L:331 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>
ORGANISM:Unknown
L:331 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:Unknown
L:331 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9, Line#:331
L:340 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Unknown
L:340 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Unknown
L:340 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10, Line#:340
L:349 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>
ORGANISM:Unknown
L:349 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>

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ORGANISM:Unknown
L:349 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:349
L:357 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>
ORGANISM:Unknown
L:357 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
ORGANISM:Unknown
L:357 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:357
L:371 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:372 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:12
L:372 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:12
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:60
L:372 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:372 M:254 E: No. of Bases conflict, LENGTH:Input:19 Counted:66 SEQ:12
L:372 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:372 M:112 C: (48) String data converted to lower case,
M:341 Repeated in SeqNo=12

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VERIFICATION SUMMARY DATE: 04/07/2006
PATENT APPLICATION: US/10/019,048A TIME: 10:25:47

Input Set : N:\SMITH\PTO.TS.14.txt
Output Set: N:\CRF4\04072006\J019048A.raw

M:254 Repeated in SeqNo=12
L:373 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13
M:112 Repeated in SeqNo=12
L:375 M:252 E: No. of Seq. differs, <211> LENGTH:Input:60 Found:82 SEQ:12
L:0 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (12)